

```

GTACGGAGGT GAGGTTTGTN ACCGCGATTG TAAGAGGTGG GCTTTTAGTC CCTCCAGACC 60
TCGGCITTAG TGCTGTCICC GCTTTTYYTT CACCTTCACA GAGGTTGCGT TCTTCCTAAA 120
AGAAGGTTTT ATTGGGAGGT AAAGGTCAAT GCGTAGGGGT AGAGTAAGAT GTCITATGGT 180
GAAATTAAAG GTAAATTCTT GGGACCTAGA GAAGAAGTAA CGAGTGAGCC ACGCTGTAAA 240
AAATTGAAGT CAACCACAGA GTCGTATGTT TTTCACAATC ATAGTAATGC TGATTTTCAC 300
AGNATCCAAG AGAAAACTGG AAATGATTGG GTCCCTGIGN NCATCATTGA TGTCAGAGGA 360
CATAGTTATT TGC 373

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FIG. 1

GTGAGGTTTG	TTACCNCGAT	TCTGAGAGGT	GGGCTTTTAG	TCCCTCCAGA	CCTCGGCTTT	60
AGTGTGTCT	CCGMTTITCT	TTCACCTTCA	CAGAGAIGTC	TIATGGTGAA	ATTGAAGTA	120
AATTCTTGGG	ACCTAGWGAA	GAAGTAAACGA	GTGAGCCACG	CTGTAAAAAA	TTGAAGTCAA	180
CCACAGAGTC	GTATGTTTTT	CACAATCATA	GTAATGCTGA	TTTTCACAGW	ATCCAAGAGA	240
AAACTGGAAA	TGATTTGGGT	CCCTIGIGACC	ATCATTNATG	TCAGAGGNCA	TAGTTAATTT	300
GCAGGAGANC	AAAAATCAAA	A				321

FIG. 2

	1				50
20483GT	GAGGTTTGT	ACCnCGATTC	TGAGAGGTGG	GCTTTTtagTC
71178	GTACGGAGGT	GAGGTTTGTn	ACCGCGATTC	TAAGAGGTGG	GCTTTTtagTC
XS7TCGACCCA	CGCGTCCGGG	GCTTTTtagTC
	51				100
20483	CCTCCAGACC	TCGGCTTTAG	TGCTGTCTCC	GNTTTTCTTT	CACCTTCACA
71178	CCTCCAGACC	TCGGCTTTAG	TGCTGTCTCC	GCTTTTNTTT	CACCTTCACA
XS7	CCTCCAGACC	TCGGCTTTAG	TGCTGTCTCC	GCTTTTCTTT	CACCTTCACA
	101				150
20483	G.....
71178	GAGGTTCGTN	TCTTCCTAAA	AGAAGGTTTT	ATTGGGAGGT	AAAGGTCAAT
XS7	GAGGTTCGTG	TCTTCCTAAA	AGAAGGTTTT	ATTGGGAGGT	AAAGGTCAAT
	151				200
20483AGAT	GTCTTATGGT	GAAATTGAAG	GTAAATTcTT
71178	GCGTAGGGGT	AGAGTAAGAT	GTCTTATGGT	GAAATTraAG	GTAAATTCTT
XS7	GCGTAGGGGT	AGAGTAAGAT	GTCTTATGGT	GAAATTGAAG	GTAAATTCTT
	201				250
20483	GGGACCTAGN	GAAGAAGTAA	CGAGTGAGCC	ACGCTGTAAA	AAATTGAAGT
71178	GGGACCTAGA	GAAGAAGTAA	CGAGTGAGCC	ACGCTGTAAA	AAATTGAAGT
XS7	GGGACCTAGA	GAAGAA....
	251				300
20483	CAACCACAGA	GTCGTATGTT	TTTCACAATC	ATAGTAATGC	TGATTTTCAC
71178	CAACCACAGA	GTCGTATGTT	TTTCACAATC	ATAGTAATGC	TGATTTTCAC
XS7CACAATC	ATAGTAATGC	TGATTTTCAC
	301				350
20483	AGNATCCAAG	AGAAAACTGG	AAATGATTTG	GGTCCCTGTG	ACCATCATTN
71178	AGNATCCAAG	AGAAAACTGG	AAATGA.TTG	GGTCCCTGTG	NNCATCATTG
xs7	AGAATCCAAG	AGAAAACTGG	AAATGA.TTG	GGTCCCTGTG	ACCATCATTG
	351				400
20483	ATGTCAGAGG	NCATAGTTAA	TTTGCAGGAG	ANCAAAAATC	AAAA.....
71178	ATGTCAGAGG	ACATAGTTAT	TT*GC.....
XS7	ATGTCAGAGG	ACATAGTTAT	TT*GCAGGAG	AACAAAATCA	AAACTACAGA
	401				450
20483
71178
XS7	TTTGCATAGAC	CTTTGCATGA	TGAGATGCCT	GGTAATAGAC	CAGATGTTA
	451			487	
20483
71178
XS7	TTGAATCCATT	GATTCACAGG	TTTTACAGGA	AGCACGT

FIG. 3

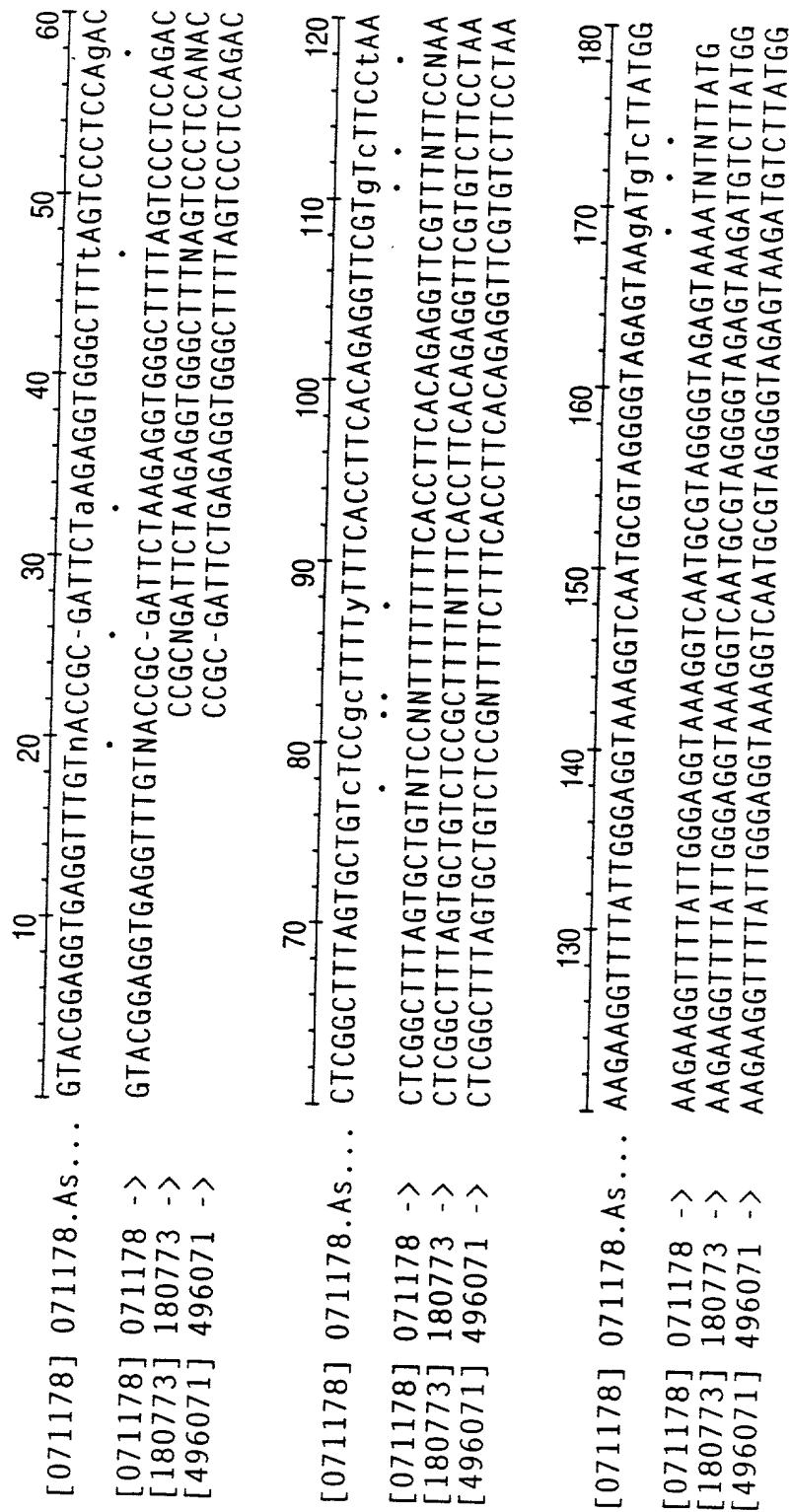


FIG. 4A

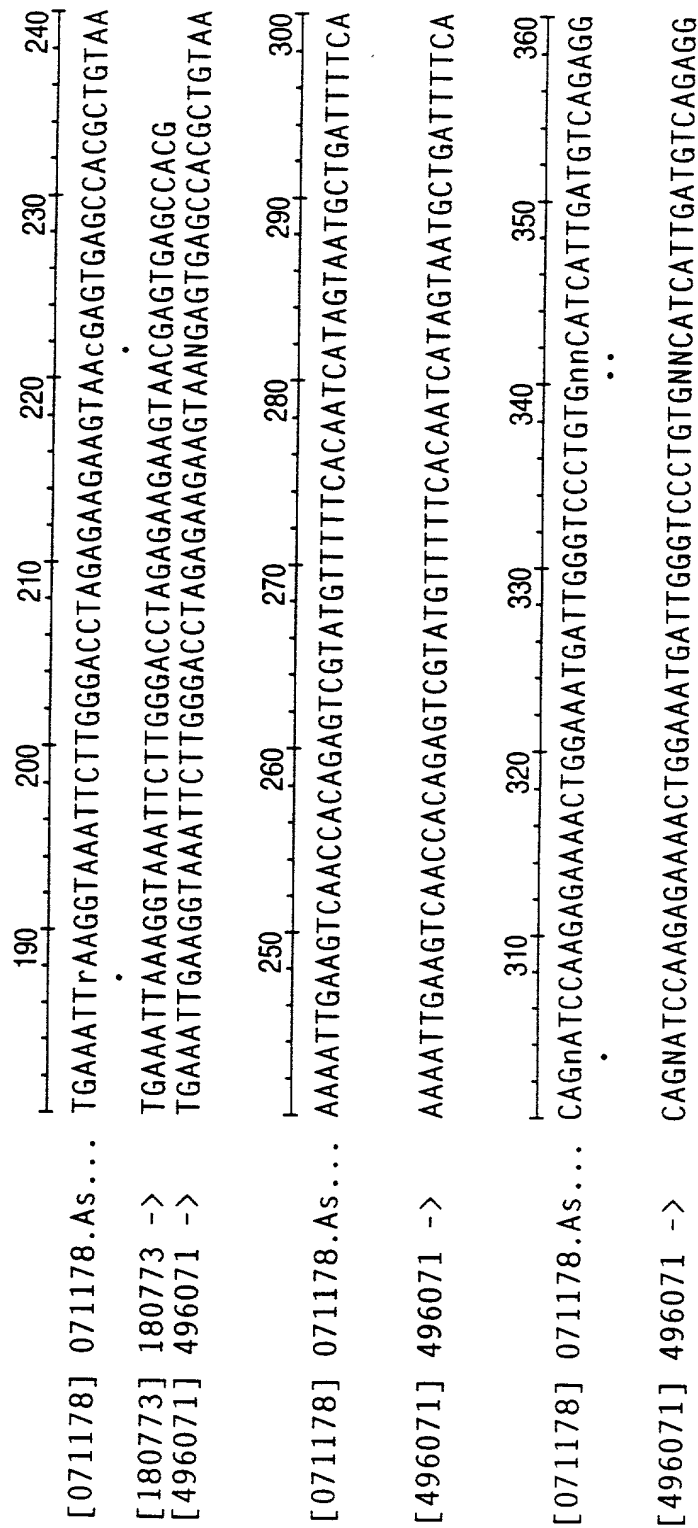


FIG. 4B

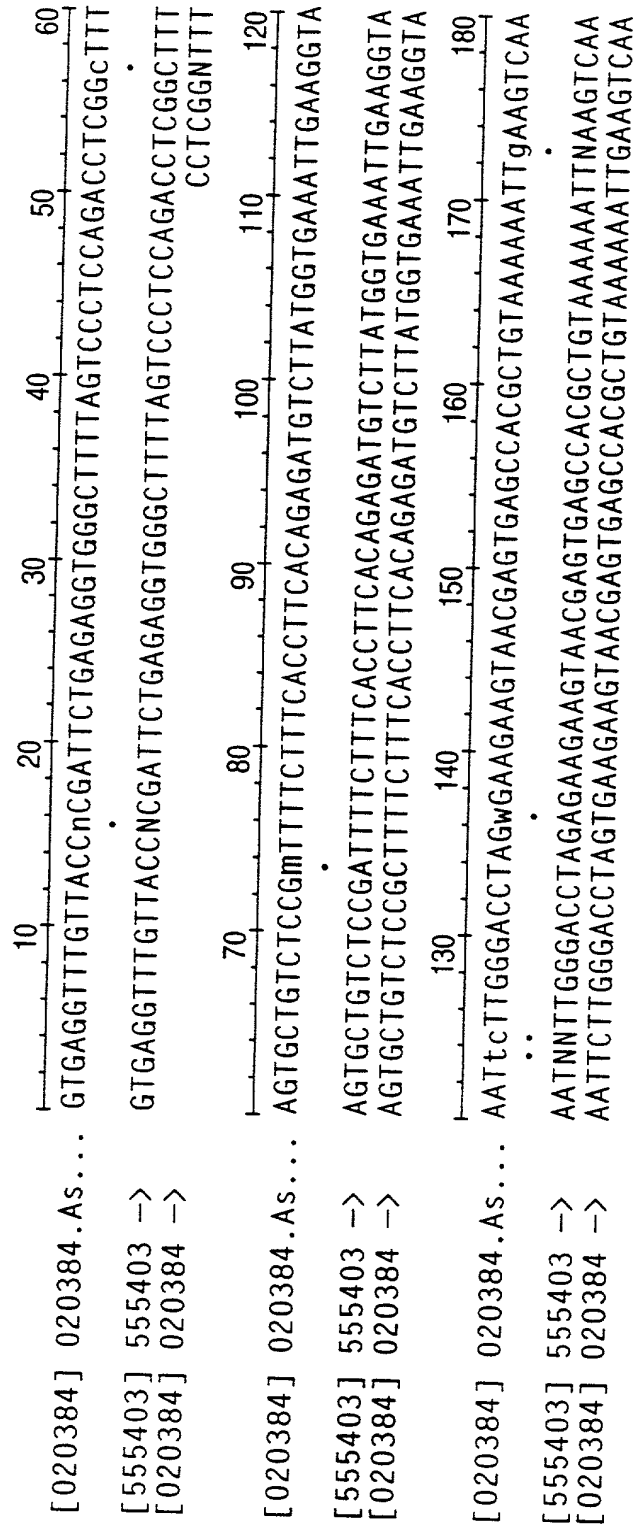


FIG. 5A

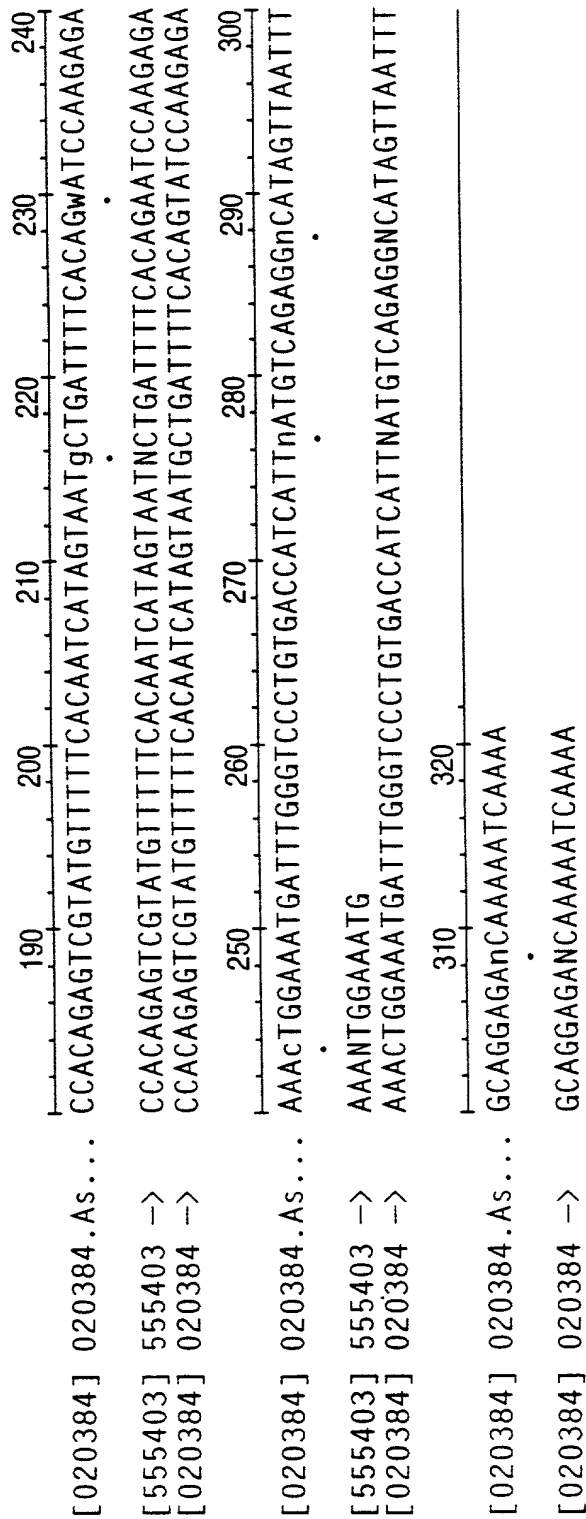


FIG. 5B

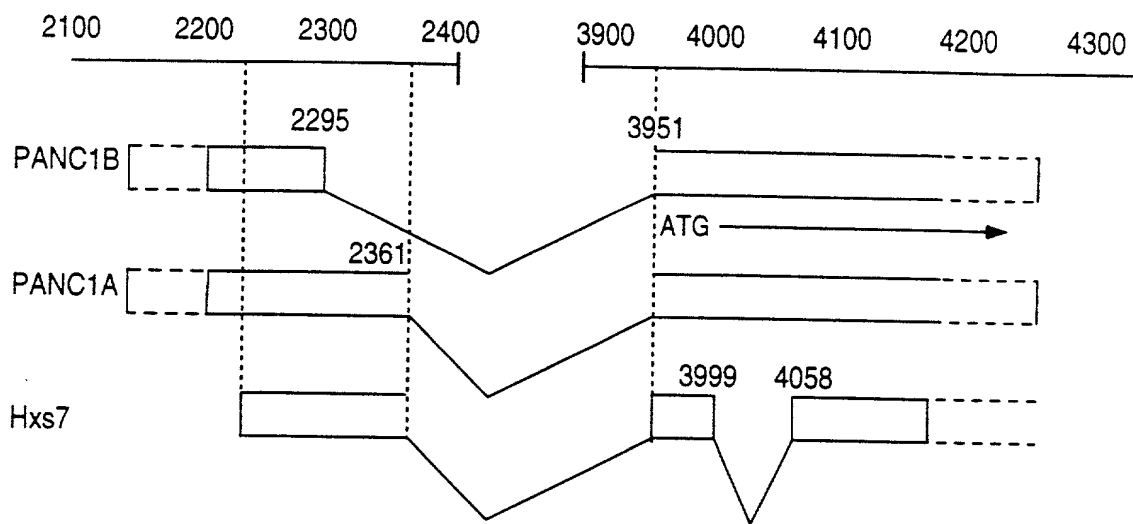


FIG. 6

PROT.PANC1A	1	VRR*GLXPRF	*EVGF*SLQT	SALVLSPLXF	HLHRGSCLPK	RRFYWEVKVN	50
PROT.XS7	DPRV	R..GF*SLQT	SALVLSPLFF	HLHRGSCLPK	RRFYWEVKVN	
PROT.PANC1B	EVCYXDSER	WAFSPSRPL*CCLXF	
	51	**					
PROT.PANC1A		A*G*SKMSYG	EIXGKFLGPR	EEVTSEPRCK	KLKSTTESYV	FHNHSNADFH	100
PROT.XS7		A*G*SKMSYG	EIEGKFLGPR	EE.....HNHSNADFH	
PROT.PANC1B		SFTFTMSYG	EIEGKFLGPX	EEVTSEPRCK	KLKSTTESYV	FHNHSNADFH	
	101						
PROT.PANC1A		XIQEKTGNDW	VPVXIIDVRG	HSYL.....	150
PROT.XS7		RIQEKTGNDW	VPVTIIDVRG	HSYLQENKIK	TTDLHRPLHD	EMPGNRPDVI	
PROT.PANC1B		XIQEKTGNDW	VPVTIIDVRG	HSVLEQXKIK	
	151						
PROT.PANC1A		162				
PROT.XS7		ESIDSQVLQE	AR				
PROT.PANC1B					

FIG. 7

SCORE = 732 (202.3 BITS), EXPECT = 5.2E-110, POISSON P(2) = 5.2E-110
IDENTITIES = 148/150 (98%), POSITIVES = 148/150 (98%), STRAND = PLUS

QUERY: 2216 CCGCGATTCTGAGAGGTGGGCTTTTAGTCCCTCCAGACCTCGGCTTTAGTGTCTCTCCG 2275
|||||
SBJCT: 1 CCGCGATTCTGAGAGGTGGGCTTTTAGTCCCTCCAGACCTCGGCTTTAGTGTCTCTCCG 60

QUERY: 2276 CTTTCTTTTCCACCTTCACAGAGGTTCGTGCTCTTCTAAAGAAGGTTTTATTGGGAGGTA 2335
|||||
SBJCT: 61 NTTTTCTTTTCCACCTTCACAGAGGTTCGTGCTCTTCTAAAGAAGGTTTTATTGGGAGGTA 120

QUERY: 2336 AAGGTCAATGCGTAGGGGTAGAGTAAGGTG 2365
|||||
SBJCT: 121 AAGGTCAATGCGTAGGGGTAGAGTAAGATG 150

FIG. 8B

>555403

LENGTH = 252

PLUS STRAND HSPS:

SCORE = 750 (207.2 BITS), EXPECT = 1.3E-53, P = 1.3E-53
IDENTITIES = 154/159 (96%), POSITIVES = 154/159 (96%), STRAND = PLUS

QUERY: 3951 AGATGCTCTTATGGTGAAATTGAAGGTAAATTCCTTGGGACCTAGAGAAGTAACGAGTG 4010
|||||
SBJCT: 94 AGATGCTCTTATGGTGAAATTGAAGGTAAATNTTGGGACCTAGAGAAGTAACGAGTG 153

QUERY: 4011 AGCCACGCTGTAAATAATTGAAGTCAACCACAGAGTCGTATGTTTTTCACAAATCATAGTA 4070
|||||
SBJCT: 154 AGCCACGCTGTAAATAATTGAAGTCAACCACAGAGTCGTATGTTTTTCACAAATCATAGTA 213

QUERY: 4071 ATGCTGATTTTCACAGAATCCAAGAGAAACTGGAAATG 4109
||
SBJCT: 214 ATNCTGATTTTCACAGAATCCAAGAGAAANTGGAAATG 252

SCORE = 458 (126.6 BITS), EXPECT = 1.1E-62, POISSON P(2) = 1.1E-62
IDENTITIES = 94/97 (96%), POSITIVES = 94/97 (96%), STRAND = PLUS

QUERY: 2203 GTGAGGTTTGTACCGCGATTCTGAGAGGTGGGCTTTTAGTCCCTCCAGACCTCGGCITT 2262
|||||
SBJCT: 1 GTGAGGTTTGTACCGCGATTCTGAGAGGTGGGCTTTTAGTCCCTCCAGACCTCGGCITT 60

QUERY: 2263 AGTGTGTCTCCGCTTTTCCTTTACCTTCACAGAGGT 2299
|||||
SBJCT: 61 AGTGTGTCTCCGATTTTCCTTTACCTTCACAGAGAT 97

FIG. 8C

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>020384
  LENGTH = 271

  PLUS STRAND HSPS:

  SCORE = 800 (221.1 BITS), EXPECT = 8.5E-58, P = 8.5E-58
  IDENTITIES = 164/169 (97%), POSITIVES = 164/169 (97%), STRAND = PLUS

  QUERY: 3951 AGATGTCCTTATGGTGAAATTGAAGGTAAATTCCTGGGACCTAGAGAAGAAGTAACGAGTG 4010
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  SBJCT: 94 AGATGTCCTTATGGTGAAATTGAAGGTAAATTCCTGGGACCTAGTGGAAGAAGTAACGAGTG 103

  QUERY: 4011 AGCCACGCTGTAAAAAATTGAAGTCAACCACAGAGTCGTATGTTTTTCACAAATCATAGTA 4070
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  SBJCT: 104 AGCCACGCTGTAAAAAATTGAAGTCAACCACAGAGTCGTATGTTTTTCACAAATCATAGTA 163

  QUERY: 4071 ATGCTGATTTTCACAGAAATCCAAGAGAAAACTGGAAATGATTGGGTCC 4119
            ||||||||||||||||||||||||||||||||||||||||||||
  SBJCT: 164 ATGCTGATTTTCACAGATATCCAAGAGAAAACTGGAAATGATTGGGTCC 212

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FIG. 8D

SCORE = 217 (60.0 BITS), EXPECT = 7.9E-20, POISSON P(2) = 7.9E-20
IDENTITIES = 45/47 (95%), POSITIVES = 45/47 (95%), STRAND = PLUS

QUERY: 2253 CCTCGGCTTTAGTGCTGTCICCGCTTTTCTTTACCTTCACAGAGGT 2299
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
SBJCT: 1 CCTCGGNTTTAGTGCTGTCICCGCTTTTCTTTACCTTCACAGAGAT 47

SCORE = 198 (54.7 BITS), EXPECT = 4.5E-28, POISSON P(3) = 4.5E-28
IDENTITIES = 42/45 (93%), POSITIVES = 42/45 (93%), STRAND = PLUS

QUERY: 4111 TTGGGTCCCTGTGACCATCATTTGATGTCAGAGGACATAGTTATTT 4155
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
SBJCT: 205 TTGGGTCCCTGTGACCATCATTTGATGTCAGAGGNCATAGTTAATT 249

FIG. 8E

>071178
LENGTH = 178
PLUS STRAND HSPS:
SCORE = 754 (208.3 BITS), EXPECT = 8.7E-54, P = 8.7E-54
IDENTITIES = 158/167 (94%), POSITIVES = 158/167 (94%), STRAND = PLUS
QUERY: 2195 GTACGGAGGTGAGGTTTGTACCGCGATTCTGAGAGGTGGGCTTTTAGTCCCTCCAGACC 2254
|||||
SBJCT: 1 GTACGGAGGTGAGGTTTGTNACCGCGATTCTAAGAGGTGGGCTTTTAGTCCCTCCAGACC 60
QUERY: 2255 TCGGCTTTAGTGCTGCTCCGCTTTTCTTTTCCACCTTCACAGAGGTCGTGCTTTCCTAAA 2314
|||||
SBJCT: 61 TCGGCTTTAGTGCTGNTCCNNTTTTTTTCACCTTCACAGAGGTCGTTTNTTCCNAAA 120
QUERY: 2315 AGAAGGTTTTATTGGGAGGTAAAGGTCAATGCCGTAGGGGTAGAGTAA 2361
|||||
SBJCT: 121 AGAAGGTTTTATTGGGAGGTAAAGGTCAATGCCGTAGGGGTAGAGTAA 167

FIG. 8F

>180773

LENGTH = 213

PLUS STRAND HSPTS:

SCORE = 685 (189.3 BITS), EXPECT = 4.0E-48; P = 4.0E-48
IDENTITIES = 141/146 (96%), POSITIVES = 141/146 (96%), STRAND = PLUS

QUERY: 2220 GATTCTGAGAGGTGGGCTTTTAGTCCCTCCAGACCTCGGCTTTAGTGTCTCCGCTTT 2279
||||| ||||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
SBJCT: 6 GATTCTAAGAGGTGGGCTTTNAGTCCCTCCANACCTCGGCTTTAGTGTCTCCGCTTT 65

QUERY: 2280 TCTTTCACCTTCACAGAGGTTCGTGTCTTCCTAAAGAGTTTTATTGGGAGGTAAAGG 2339
| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
SBJCT: 66 TTTTTCACCTTCACAGAGGTTCGTGTCTTCCTAAAGAGTTTTATTGGGAGGTAAAGG 125

QUERY: 2340 TCAATGCGTAGGGGTAGAGTAAGGTG 2365
||||||| ||||||||| ||||||||| ||
SBJCT: 126 TCAATGCGTAGGGGTAGAGTAAGATG 151

SCORE = 327 (90.4 BITS), EXPECT = 3.0E-39, POISSON P(2) = 3.0E-39
IDENTITIES = 67/69 (97%), POSITIVES = 67/69 (97%), STRAND = PLUS

QUERY: 3949 TCAGATGTCTTATGGTGAAATTGAAGGTAAATTTCTTGGGACCTAGAGAAAGTAACGAG 4008
| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
SBJCT: 145 TAAGATGTCTTATGGTGAAATTGAAGGTAAATTTCTTGGGACCTAGAGAAAGTAACGAG 204

QUERY: 4009 TGAGCCACG 4017
|||||||
SBJCT: 205 TGAGCCACG 213

FIG. 8G

5'	9	18	27	36	45	54
	CCG CGA TTC TGA GAG GTG GGC TTT TAG TCC CTC CAG ACC TCG GCT TTA GTG CTG					
	63	72	81	90	99	108
	TCT CCG CTT TTC TTT CAC CTT CAC AGA GGT TCG TGT CTT CCT AAA AGA AGG TTT					
	117	126	135	144	153	162
	TAT TGG GAG GTA AAG GTC AAT GCG TAG GGG TAG AGT AAG ATG TCT TAT GGT GAA					
					M S Y G E	
	171	180	189	198	207	216
	ATT GAA GGT AAA TTC TTG GGA CCT AGA GAA GTA ACG AGT GAG CCA CGC TGT					
	I E G K F L G P R E V T S E P R C					
	225	234	243	252	261	270
	AAA AAA TTG AAG TCA ACC ACA GAG TCG TAT GTT TTT CAC AAT CAT AGT AAT GCT					
	K K L K S T T E S Y V F H N S N A					
	279	288	297	306	315	324
	GAT TTT CAC AGA ATC CAA GAG AAA ACT GGA AAT GAT TGG GTC CCT GTG ACC ATC					
	D F H R I Q E K T G N D W V T					
	333	342	351	360	369	378
	ATT GAT GTC AGA GGA CAT AGT TAT TTG CAG GAG AAC AAA ATC AAA ACT ACA GAT					
	I D V R G H S Y L Q E N K I K T T D					

FIGURE 9A

387	396	405	414	423	432
TTG CAT AGA CCT TTG CAT GAT GAG ATG CCT GGT AAT AGA CCA GAT GTT ATT GAA					
L H R P L H D E M P G N R P D V I E					
441	450	459	468	477	486
TCC ATT GAT TCA CAG GTT TTA CAG GAA GCA CGT CCT CCA TTA GTA TCC GCA GAC					
S I D S Q V L Q E A R P P L V S A D					
495	504	513	522	531	540
GAT GAG ATA TAT AGC ACA AGT AAA GCA TTT ATA GGA CCC ATT TAC AAA CCC CCT					
D E I Y S T S K A F I G P I Y K P P					
549	558	567	576	585	594
GAG AAA AAG AAA CGT AAT GAA GGG AGG AAT GAG GCA CAT GTT CTA AAT GGT ATA					
E K K K R N E G R N E A H V L N G I					
603	612	621	630	639	648
AAT GAC AGA GGA GGA CAA AAA GAG AAA CAG AAA TTT AAC TCT GAA AAA TCA GAG					
N D R G G Q K E K Q K F N S E K S E					
657	666	675	684	693	702
ATT GAC AAT GAA TTA TTC CAG TTT TAC AAA GAA ATT GAA GAG CTT GAA AAG GAA					
I D N E L F Q F Y K E I E E L E K E					
711	720	729	738	747	756
AAA GAT GGT TTT GAG AAC AGT TGT AAA GAA TCT GAA CCT TCT CAG GAA CAA TTT					
K D G G F E N S C K E S E P S Q E Q F					

FIGURE 9B

765	774	783	792	801	810
GTT CCA TTT TAT GAG GGT CAT AAT AAT GGT CTC TTA AAA CCT GAT GAA GAA AAG					
V P F Y E G H N N G L L K P D E E K					
819	828	837	846	855	864
AAA GAT CTT AGT AAT AAA GCT ATG CCA TCA CAT TGT GAT TAT CAG CAG AAC TTG					
K D L S N K A M P S H C D Y Q Q N L					
873	882	891	900	909	918
GGG AAT GAG CCA GAC AAA TAT CCC TGT AAT GGA CAA GTA ATA CCT ACA TTT TGT					
G N E P D K Y P C N G Q V I P T F C					
927	936	945	954	963	972
GAC ACT TCA TTT ACT TCT TTC AGG CCT GAA TGG CAG TCA GTA TAT CCT TTT ATA					
D T S F T S F R P E W Q S V Y P F I					
981	990	999	1008	1017	1026
GTG CCC TAT GGT CCC CCT CTT CCC AGT TTG AAC TAT CAT TTA AAC ATT CAG AGA					
V P Y G P P P L P S L N Y H L N I Q R					
1035	1044	1053	1062	1071	1080
TTC AGT GGT CCA CCA AAT CCA CCA TCA AAT ATT TTC CAA GCC CAA GAT GAC TCT					
F S G P P N P P S N I F Q A Q D D S					
1089	1098	1107	1116	1125	1134
CAG ATA CAA AAT GGA TAT TAT GTA AAT AAT TGT CAT GTT AAC TGG AAT TGC ATG					
Q I Q N G Y Y V N N C H V N W N C M					

FIGURE 9C

1143	1152	1161	1170	1179	1188
ACT TTT GAT CAG AAC AAT GAA TAT ACT GAC TGT AGT GAG AAT AGG AGT AGT GTT					
T F D Q N N E Y T D C S E N R S S V					
1197	1206	1215	1224	1233	1242
CAT CCC TCT GGA AAT GGC TGC AGT ATG CAA GAT CGA TAT GTG AGT AAT GGT TTC					
H P S G N G C S M Q D R Y V S N G F					
1251	1260	1269	1278	1287	1296
TGT GAA GTC AGA GAA AGA TGC TGG AAA GAT CAT TGT ATG GAC AAG CAT AAT GGA					
C E V R E R C W K D H C M D K H N G					
1305	1314	1323	1332	1341	1350
ACA GAC AGG TTT GTG AAC CAG CAG TTT CAA GAG GAA AAG TTA AAT AAA TTG CAG					
T D R F V N Q Q F Q E E K L N K L Q					
1359	1368	1377	1386	1395	1404
AAG TTA CTT ATT CTT TTA AGA GGT CTG CCT GGT TCT GGG AAA ACA ACA TTG TCT					
K L L I L L R G L P G S G K T T L S					
1413	1422	1431	1440	1449	1458
CGA ATT CTG CTT GGT CAG AAT CGT GAT GGC ATT GTG TTC AGC ACT GAT GAC TAT					
R I L L G Q N R D G I V F S T D Y					
1467	1476	1485	1494	1503	1512
TTT CAC CAT CAA GAT GGG TAC AGG TAT AAT GTT AAT CAA CTT GGT GAT GCC CAT					
F H H Q D G Y R Y N V N Q L G D A H					

FIGURE 9D

1521	1530	1539	1548	1557	1566
GAC TGG AAC CAG AAC AGA GCA AAA GCT ATC GAT CAG GGA AGA TCT CCA GTT					
D W N Q N R A K Q A I D Q G R S P V					
1575	1584	1593	1602	1611	1620
ATA ATA GAT AAC ACT AAT ATA CAA GCT TGG GAA ATG AAG CCA TAT GTG GAA GTG					
I I D N T N I Q A W E M K P Y V E V					
1629	1638	1647	1656	1665	1674
GCC ATA GGA AAA GGA TAC AGA GTA GAG TTT CAT GAA CCT GAA ACT TGG TGG AAA					
A I G K G Y R V E F H E P E T W K					
1683	1692	1701	1710	1719	1728
TTT GAT CCT GAA GAA TTA GAA AAG AGG AAT AAA CAT GGT GTG TCT CGA AAG AAG					
F D P E E L E K R N K H G V S R K K					
1737	1746	1755	1764	1773	1782
ATT GCT CAG ATG TTG GAT CGT TAT GAA TAT CAA ATG TCC ATT TCT ATT GTA ATG					
I A Q M L D R Y E Y Q M S I S I V M					
1791	1800	1809	1818	1827	1836
AAT TCA GTG GAA CCA TCA CAC AAA AGC ACA CAA AGA CCT CCT CCT CCA CAG GGG					
N S V E P S H K S T Q R P P P P Q G					
1845	1854	1863	1872	1881	1890
AGA CAG AGG TGG GGA GGC TCT CTT GGC TCA CAT AAT CGT GTC TGT GTC ACA AAT					
R Q R W G G S L G S H N R V C V T N					

FIGURE 9E

1899	1908	1917	1926	1935	1944
AAT CAT TAA ATT AGC TAT TTT CAG CTA ACA CAT TTG TTG CAC TTG AAA AAG					
N H					
1953	1962	1971	1980	1989	1998
AGT TAG TGA GCC TGT CTT GGA GTT TAA GTA GTT TCA AAT AAA AAA AGG CTA CAG					

FIGURE 9F

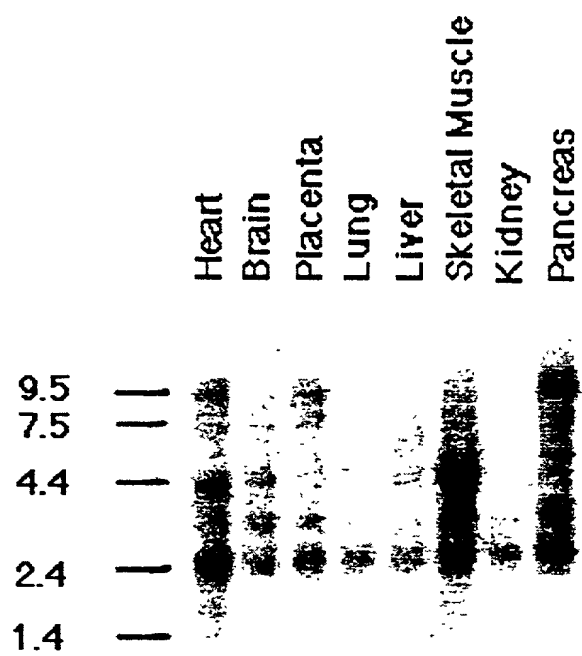


FIGURE 10A

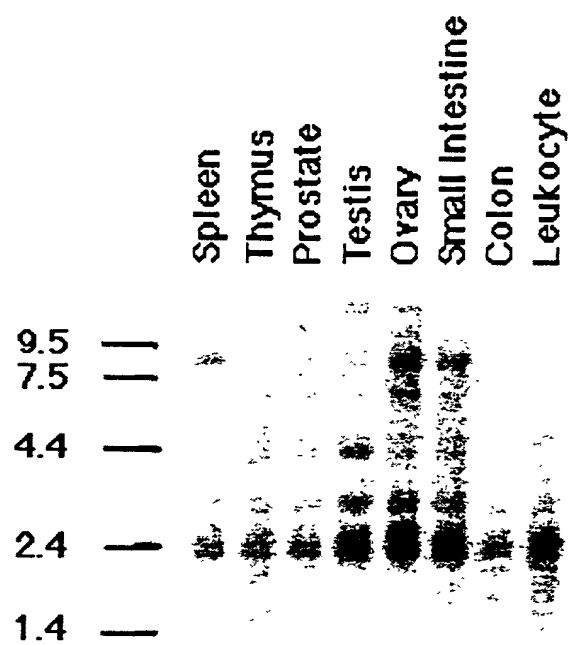


FIGURE 10B